

178363

From: Chernyshev, Olga  
Sent: Wednesday, February 01, 2006 2:20 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/815,297, sequence search request

Please search SEQ ID NO: 3 down to 60% identity in regular databases only.  
Thank you very much!

Olga N. Chernyshev, Ph.D.  
AU 1649  
REM 3C89  
2-0870  
mail 4C70

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA#: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

## OM protein - protein search, using sw model

Run on: February 7, 2006, 20:47:32 ; Search time 17 Seconds  
 (without alignments)  
 375.667 Million cell updates/sec

Title: US-10-815-297-3  
 Perfect score: 2872

Sequence: 1 MLKQSERRSWSYRPWNTE.....KKIAECILGSNPQLTPRQEN 545

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext: 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60% )  
 Maximum Match 100% summaries  
 Listing first 500 summaries

Database : Published Applications AA New:\*

```

1: /cgns_6/prodata/2/pubpaas/US09_NEW_PUB.pep:*
2: /cgns_6/prodata/2/pubpaas/US06_NEW_PUB.pep:*
3: /cgns_6/prodata/2/pubpaas/US07_NEW_PUB.pep:*
4: /cgns_6/prodata/2/pubpaas/PCT_NEW_PUB.pep:*
5: /cgns_6/prodata/2/pubpaas/US09_NEW_PUB.pep:*
6: /cgns_6/prodata/2/pubpaas/US10_NEW_PUB.pep:*
7: /cgns_6/prodata/2/pubpaas/US11_NEW_PUB.pep:*
8: /cgns_6/prodata/2/pubpaas/US60_NEW_PUB.pep:*
```

6 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
-----	-----	-----	-----	-----

No matches found

Search completed: February 7, 2006, 20:50:43  
 Job time : 17 secs



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## ON Protein - protein search, using SW model

Run on: February 7, 2006, 20:46:31 ; Search time 180 Seconds

1265.094 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: I MLKQSERRSWSYRPWNTE.....KKIAECLIGSNPQLTPRQEN 545

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60% )

Maximum Match 100% )

Listing first 500 summaries

Database : Published Applications AA Min:\*

1: /cgns\_6/ptoda/a/1/pupbaa/us07\_pubcomb.pep: \*

2: /cgns\_6/ptoda/a/1/pupbaa/us08\_pubcomb.pep: \*

3: /cgns\_6/ptoda/a/1/pupbaa/us09\_pubcomb.pep: \*

4: /cgns\_6/ptoda/a/1/pupbaa/us10\_pubcomb.pep: \*

5: /cgns\_6/ptoda/a/1/pupbaa/us11\_pubcomb.pep: \*

6: /cgns\_6/ptoda/a/1/pupbaa/us11\_pubcomb.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Match Length	DB ID	Description
1	2872	100.0	545	3	US-09-918-359-2 Sequence 2, Appli
2	2872	100.0	545	3	US-09-918-359-3 Sequence 3, Appli
3	2872	100.0	545	4	US-10-815-297-3 Sequence 4, Appli
4	2862	99.7	545	3	US-09-919-220B-36 Sequence 5, Appli
5	2857	99.5	545	3	US-09-999-220B-116 Sequence 6, Appli
6	2849	99.2	545	3	US-09-999-220B-120 Sequence 7, Appli
7	2803.5	97.6	662	4	US-09-999-220B-24 Sequence 8, Appli
8	2781	96.8	545	3	US-09-999-220B-34 Sequence 9, Appli
9	2778	96.7	545	3	US-09-999-220B-118 Sequence 10, Appli
10	2401	83.6	467	4	US-10-114-270-44 Sequence 11, Appli

## ALIGNMENTS

RESULT 1  
US-09-918-359-2  
; Sequence 2, Application US 06918359  
; Publication No. US0030064490A1  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Mathur, Brian  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Priddle, Carl Johan  
; APPLICANT: Gerhardt, Brenda  
; TITLE OF INVENTION: Novel Human Ion Channel Proteins and Polynucleotides Encoding the

RESULT 2  
US-09-833-466-3  
; Sequence 3, Application US 09833466  
; Publication No. US20040053357A1  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy James  
; APPLICANT: ICager, Inc.  
; TITLE OF INVENTION: K10.1, a No. US20040053357A1 Voltage-Gated Potassium Channel F  
; FILE REFERENCE: 018512-005100US  
; CURRENT APPLICATION NUMBER: US/09/833, 466

PRIOR APPLICATION NUMBER: US 60/197,793  
PRIOR FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human alpha subunit  
OTHER INFORMATION: channel Kv10.1  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (102)..(514)  
OTHER INFORMATION: conserved region of  
OTHER INFORMATION: channel Kv10.1  
S-09-833-466-3

PRIOR APPLICATION NUMBER: US 60/197,793  
PRIOR FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human alpha subunit of voltage-gated potassium  
OTHER INFORMATION: channel Kv10.1  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (102)..(514)  
OTHER INFORMATION: conserved region of voltage-gated potassium  
OTHER INFORMATION: channel Kv10.1  
US-09-833-466-3

CURRENT APPLICATION NUMBER: US/10/815,297  
CURRENT FILING DATE: 2004-03-31  
PRIOR APPLICATION NUMBER: US/09/633,466  
PRIOR FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: US 60/197,793  
PRIOR FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human alpha subunit of voltage-gated potassium  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (102) (514)

CURRENT APPLICATION NUMBER: US10/815,297  
CURRENT FILING DATE: 2004-03-31  
PRIORITY APPLICATION NUMBER: US/09/833,466  
PRIORITY FILING DATE: 2001-04-11  
PRIORITY APPLICATION NUMBER: US 60/197,793  
PRIORITY FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 545  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human alpha subunit of voltage-gated potassium  
OTHER INFORMATION: channel Kv1.0.1  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATOR: (102) (51A)

Query	Match	Score	DB	Length	545;
	Best Local Similarity	100.0%	Pred.	No.	5..9e-265;
	Matches	45;	Conservative	0;	Mismatches
			Indels	0;	Gaps
				0;	0;
Qy	1 MLKOSERRESWSYPPWNTTENEGSQRHSRSTCSGRSGOASHTGWTGTYNTYEEBD	60			
	1 MLKGSERRSWSYPPWNTTENEGSQRHSRSTCSGRSGOASHTGWTGTYNTYEEBD	60			
Qy	61 GEEBDQWQDQDAEEDQQAGETVTTAKPEGSDPPALIUSTINVNQGHGSYOLDYCCELLAGFPK	120			
	61 GEEBDQWQDQDAEEDQQAGETVTTAKPEGSDPPALIUSTINVNQGHGSYOLDYCCELLAGFPK	120			
Db	121 TRIGRLATSTSRSQQLCDDYEQSTDYEFDRDPAVFOLVNFYLQSVLVLIDGLCPER	180			
	121 TRIGRLATSTSRSQQLCDDYEQSTDYEFDRDPAVFOLVNFYLQSVLVLIDGLCPER	180			
Qy	181 FLEGLGYWGURLKTPRCCRICPERRDELSERLUKIQHBLRAQVBEABLERFDMDRFG	240			
	181 FLEGLGYWGURLKTPRCCRICPERRDELSERLUKIQHBLRAQVBEABLERFDMDRFG	240			
Qy	241 PORRLWNLMKEPKFSSVAAKAIGAVSSTFLVSVALANTVNEEMQHQSGOGEGGPDLRP	300			
	241 PORRLWNLMKEPKFSSVAAKAIGAVSSTFLVSVALANTVNEEMQHQSGOGEGGPDLRP	300			
Db	301 ILETHVEMLGPFTEYLRLASTPDLRRPARSAINVLDIVAILPELYQILLCFFGECH	360			
	301 ILETHVEMLGPFTEYLRLASTPDLRRPARSAINVLDIVAILPELYQILLCFFGECH	360			
Qy	361 ORGQTVGSGVKVGQVLVRMLMRFRILKLAHRHSTGLRAGFTLRQCYQVGCLLFIAM	420			
	361 ORGQTVGSGVKVGQVLVRMLMRFRILKLAHRHSTGLRAGFTLRQCYQVGCLLFIAM	420			
Db	421 GIFTSAAVSVHEVDUPSTNFTTPIHSMWAASVSTVGJGDMPEBTHGRFPLCIAF	480			
	421 GIFTSAAVSVHEVDUPSTNFTTPIHSMWAASVSTVGJGDMPEBTHGRFPLCIAF	480			
Qy	481 GIILNGMPISILYNKFSYDYSKLUKAYEVTIRREGEVNFMQRARKKIAECUCLGSSNPOLT	540			
	481 GIILNGMPISILYNKFSYDYSKLUKAYEVTIRREGEVNFMQRARKKIAECUCLGSSNPOLT	540			
Qy	541 PROEN 545				
Db	541 PROEN 545				

DOCUMENT: 1127...J44  
 OTHER INFORMATION: conserved region of voltage-gated potassium  
 ; OTHER INFORMATION: channel Kv10.1  
 ; US-10-815-297-3

Query Match	Best Local Similarity	Score	DB	Length	
QY	100 %;	Score 2872;	4	Length 545;	
	Best Local Similarity	100 %;	Pred. No.	5_9e-265;	
	Matches	0;	Mismatches	0;	
	545;	Conservative	0;	Indels	0;
				Gaps	0;
Qy	1	MLKQSERRRSWSYRPMTTENGSQRRSICSLGAGSQASHINGTEGNYYIEDED	60		
Db	1	MLKQSERRRSWSYRPMTTENGSQRRSICSLGAGSQASHINGTEGNYYIEDED	60		
Qy	61	GEREDEDQKDDLABEDDQAGEVTTAKPGPSDOPALASTLNNAVGGSYOLDYCCELAGFPK	120		
Db	61	GEREDEDQKDDLABEDDQAGEVTTAKPGPSDOPALASTLNNAVGGSYOLDYCCELAGFPK	120		
Qy	121	TRGRLATSTSRSRQLSCLDDEYEQDYEYFDRDPAPVOLVNFYASGLVLTLDGCPRR	180		
Db	121	TRGRLATSTSRSRQLSCLDDEYEQDYEYFDRDPAPVOLVNFYASGLVLTLDGCPRR	180		
Qy	181	FLEELGGWGVRLKXTPRCCRCLFEERDELSERLKQHRLAQAOQEAEELFRDRPYG	240		
Db	181	FLEELGGWGVRLKXTPRCCRCLFEERDELSERLKQHRLAQAOQEAEELFRDRPYG	240		
Qy	241	PORRRLNLMKEPPSSVAKAIGVASSTEPVLSVWVALNTVEEMOHSOGCGEGGDLRP	300		
Db	241	PORRRLNLMKEPPSSVAKAIGVASSTEPVLSVWVALNTVEEMOHSOGCGEGGDLRP	300		
Qy	301	IIEHVMCMGPFITLEVILRLASTPDIRPARSALINVDVIALPLYLQIUCFCFGH	360		
Db	301	IIEHVMCMGPFITLEVILRLASTPDIRPARSALINVDVIALPLYLQIUCFCFGH	360		
Qy	361	QRSOTVGSVKGKVQVLRVNLARIFRKLRHSTGRAFTLRCYQQVGCCLIFTAM	420		
Db	361	QRSOTVGSVKGKVQVLRVNLARIFRKLRHSTGRAFTLRCYQQVGCCLIFTAM	420		
Qy	421	GIFTPSAVVSYEHDVSTINFTTIPHSWWAAVSISTWGYGDMYPELTLGRPFACIAF	480		
Db	421	GIFTPSAVVSYEHDVSTINFTTIPHSWWAAVSISTWGYGDMYPELTLGRPFACIAF	480		
Qy	481	GITLNGMPITSILYNKFSDYSSKLKAYEVTTIRRERGVNFMORARKKIAECILGSNQLT	540		
Db	481	GITLNGMPITSILYNKFSDYSSKLKAYEVTTIRRERGVNFMORARKKIAECILGSNQLT	540		
Qy	541	PROBN 545			
Db	541	PROBN 545			

Sequence 3, Application US 18115297  
Publication No. US20040157261A1  
GENERAL INFORMATION:  
APPLICANT: Jegla, Timothy James  
APPLICANT: ICAEN, Inc.  
TITLE OF INVENTION: Kv10.1, a Novel Voltage-Gated Potassium Channel From Human Brain  
FILE REFERENCE: 018512-005910US

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on:

February 7, 2006, 20:45:41 ; Search time 51 Seconds

883.495 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: 1 MLKQSERRSRWSYRPWNTTE . . . . . KKIACCLGSNPOLTPRQEN 545

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 572060 seqb, 82675679 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 60%

Listing first 500 summaries

Database : Issued Patents AA,\*

1: /cgtr2\_6/ptodata/1/1aa/5\_COMB\_pep: \*  
 2: /cgtr2\_6/ptodata/1/1aa/6\_COMB\_pep: \*  
 3: /cgtr2\_6/prodata/1/1aa/H\_COMB\_pep: \*  
 4: /cgtr2\_6/prodata/1/1aa/PCUS\_COMB\_pep: \*  
 5: /cgtr2\_6/ptodata/1/1aa/RG\_COMB\_pep: \*  
 6: /cgtr2\_6/prodata/1/1aa/backfilesl\_pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2872	(C) 100.0	545	2	US-09-833-466-3

Sequence 3, Appli

## ALIGNMENTS

RESULT 1 US-09-833-466-3

Sequence 3 Application US/09833466

Patent No. 672353

GENERAL INFORMATION:

APPLICANT: Jegla, Timothy James

APPLICANT: ICagen, Inc.

TITLE OF INVENTION: KV10.1, a No. 6727353el Voltage-Gated Potassium Channel From

TITLE OF INVENTION: Human Brain

FILE REFERENCE: 018512-005910US

CURRENT APPLICATION NUMBER: US/09-833,466

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: US 60/197,793

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 3

LENGTH: 545

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human alpha subunit of voltage-gated potassium  
 OTHER INFORMATION: channel Kv10.1  
 FEATURE:  
 NAME/KEY: PEPTIDE  
 LOCATION: (102)..(514)  
 OTHER INFORMATION: conserved region of voltage-gated potassium

OTHER INFORMATION: channel Kv10.1

US-09-833-466-3

Query Match 100.0%; Score 2872; DB 2; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-294;  
 Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKQSERRSRWSYRPWNTTE . . . . . KKIACCLGSNPOLTPRQEN 545  
 Db 1 MLKQSERRSRWSYRPWNTTE . . . . . KKIACCLGSNPOLTPRQEN 545

Qy 61 GREEEDWKDIAERDQAGETTAKEPREGSDPPALISTLNNGHHSYQDJYCELAGFPK 120  
 Db 61 GEEEDWKDIAERDQAGETTAKEPREGSDPPALISTLNNGHHSYQDJYCELAGFPK 120

Qy 121 TRLGRLATTSRSRQLSLCDYEQTDEYTFDRDAVFLQVNFILGVVLLDGLCP 180  
 Db 121 TRLGRLATTSRSRQLSLCDYEQTDEYTFDRDAVFLQVNFILGVVLLDGLCP 180

Qy 181 FLEELGYWGVRKYTPRCCRCCFEERDELSERKIQHELRQAQVEAEELFRDMRFYQ 240  
 Db 181 FLEELGYWGVRKYTPRCCRCCFEERDELSERKIQHELRQAQVEAEELFRDMRFYQ 240

Qy 241 PORRRLINLNEKPEFSSVAIAVGASSTEVLSVVALAALVTEEMQHQSGEGSPDPRLP 300  
 Db 241 PORRRLINLNEKPEFSSVAIAVGASSTEVLSVVALAALVTEEMQHQSGEGSPDPRLP 300

Qy 301 ILEHVELMCMGPFTLEYLRLASTDPRRPARSALNLVDVAILPLYQOLLECTGECH 360  
 Db 301 ILEHVELMCMGPFTLEYLRLASTDPRRPARSALNLVDVAILPLYQOLLECTGECH 360

Qy 361 ORGQTGVSGVKVGQVIRVMRLMRFLKLARHSTGLRAFGFTLROCYQQGCLLPIAM 420  
 Db 361 ORGQTGVSGVKVGQVIRVMRLMRFLKLARHSTGLRAFGFTLROCYQQGCLLPIAM 420

Qy 421 GIFTSAVSVEHDPSTNFTTIPHSWWNAVSISTVGYGDMPYBTHIGRFFAFLIAF 480  
 Db 421 GIFTSAVSVEHDPSTNFTTIPHSWWNAVSISTVGYGDMPYBTHIGRFFAFLIAF 480

Qy 481 GILNGMPISLYNKEDSYSKLUAYTITRREGEVNIMQRKKAECCLGSNPQLT 540  
 Db 481 GILNGMPISLYNKEDSYSKLUAYTITRREGEVNIMQRKKAECCLGSNPQLT 540

Search completed: February 7, 2006, 20:47:16

Job time : 51 secs



GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: February 7, 2006, 20:38:06 ; Search time 249 Seconds

(without alignments) 1544.229 Million cell updates/sec

Title: US-10-815-297-3

Perfect score: 2872

Sequence: 1 M<sub>L</sub>KQSERRRSSWSYRPWNTE.....KKIAECLIGSNPQLTPRQEN 545

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

## Searched:

2166443 seqs, 705528306 residues

## Total number of hits satisfying chosen parameters:

3

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%, Maximum Match 100%

Listing first 500 summaries

Database : UniProt\_05.80;\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2872	100.0	545	1 KCNV2_HUMAN	08tdn2 homo sapien
2	2872	100.0	545	2 Q8T6X0_HUMAN	05t6x0 homo sapien
3	2302.5	80.2	562	2 Q8cf86_MOUSE	Q8cf86 mus musculus

## ALIGNMENTS

RESULT 1	KCNV2_HUMAN	STANDARD;	PRT;	545 AA.
ID	KCNV2_HUMAN			
AC	Q8TDN2_HUMAN			
DT	28-FEB-2003 (Rel. 4.1, Created)			
DT	28-FEB-2003 (Rel. 4.1, Last sequence update)			
DT	10-MAY-2005 (Rel. 4.7, Last annotation update)			
DE	potassium voltage-gated channel subfamily V member 2 (voltage-gated potassium channel subunit Kv8.2).			
DE	Name=KCNV2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo;			
OC	NCBI_TAXID=9606;			
RN	{1}			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain;			
RC	MEDLINE=2205608; PubMed=12060745; DOI=10.1073/pnas.122617999;			
RA	Ottschytach N., Raes A., Van Hoornick D., Snyder D.J.;			
RT	"Obligatory heterotrimerization of three previously uncharacterized Kv channel alpha-subunits identified in the human genome.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:7986-7991(2002).			

-I- FUNCTION: Potassium channel subunit. Modulates channel activity by shifting the threshold and the half-maximal activation to more negative values.

-I- SUBUNIT: Heterotrimer with KCNBL1, KCNCl and KCNF1. Does not form homomultimers.

-I- TISSUE SPECIFICITY: Detected in lung, liver, kidney, pancreas, spleen, thymus, prostate, testis, ovary and colon.

-I- DOMAIN: The segment S4 is probably the voltage-sensor and is associated with KCNBL1 or possibly another partner to be inserted in the plasma membrane. Remains intracellular in the absence of KCNBL1.

-I- SUBCELLULAR LOCATION: Integral membrane protein. Has to be characterized by a series of positively charged amino acids at every third position.

-I- SIMILARITY: Belongs to the potassium channel family. V subfamily.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

Ensembl; ENSG0000168263; Homo sapiens.

HGNC; HGNC:19688; KCNV2.

MIM: 607604; -

InterPro; IPR005821; Ion trans.

InterPro; IPR003091; K+channel.

InterPro; IPR003968; Kv Channel.

InterPro; IPR005820; M+Channel\_ng.

Pfam; PF00520; Ion\_trans\_1.

Pfam; PF02214; K\_tetra\_1.

PRINTS; PRO1494; KVCHANNEL.

PRINTS; PRO167; KVCHANNEL.

KW Glycoprotein; Ion transport; Ionic channel; Multigene family;

KW Potassium; Potassium channel; Potassium transport; Transmembrane;

KW Transport; Voltage-gated channel.

PTP TOPO\_DOM 1 155 Cytoplasmic (Potential).

PTP TRANSMEM 156 176 Segment S1 (Potential).

PTP TRANSMEM 262 282 Segment S2 (Potential).

PTP TOPO\_DOM 283 336 Cytoplasmic (Potential).

PTP TRANSMEM 337 357 Segment S3 (Potential).

PTP TRANSMEM 375 395 Segment S4 (Potential).

PTP TRANSMEM 396 410 Cytoplasmic (Potential).

PTP TRANSMEM 411 431 Segment S5 (Potential).

PTP TRANSMEM 472 492 Segment S6 (Potential).

PTP TOPO\_DOM 493 545 Cytoplasmic (Potential).

PTP REGION 445 465 Segment H5 (pore-forming) (Potential).

PTP MOTIF 457 462 Selectivity filter (By Similarity).

PTP CARBOHYD 440 440 N-linked (GlycNAc, .) (Potential).

PTP SEQUENCE 545 AA; 62459 MW; 72D175B4C06B1DA CRC64;

Query Match Similarity 100.0%; Score 2872; DB 1; Length 545;

Matches 545; Conservative 0; Misaligned 0; Indexes 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.7e-219;

Matches 545; Conservative 0; Misaligned 0; Indexes 0; Gaps 0;

1 MILKQSERRRSSWSYRPWNTE.....KKIAECLIGSNPQLTPRQEN 545

QY 181 FLEELGYWGRVLRKYTPRCCRCFEEERDESERLKLQHELAQAOQEAEELFRDMRFYG 240  
 Db 181 FLEELGYWGRVLRKYTPRCCRCFEEERDESERLKLQHELAQAOQEAEELFRDMRFYG 240  
 QY 241 PORRLMLMKPFPSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300  
 Db 241 PORRLMLMKPFPSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300  
 QY 301 ILEHVELCMGFFTLEYLLASTPDIRFARSALNLVLDVAILPLXJQLLBCFTGEH 360  
 Db 301 ILEHVELCMGFFTLEYLLASTPDIRFARSALNLVLDVAILPLXJQLLBCFTGEH 360  
 QY 361 ORGOTGVSGVKQVLRLMRIRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420  
 Db 361 ORGOTGVSGVKQVLRLMRIRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420  
 QY 421 GIFTPSAVSVEHDVPSNTFTIPHSWWMAVSISVGSDMYPETHLGRFAFLCAF 480  
 Db 421 GIFTPSAVSVEHDVPSNTFTIPHSWWMAVSISVGSDMYPETHLGRFAFLCAF 480  
 QY 481 GILNGMPISILYNKFSDYYSKLAKAYEYTIRRERGEVNFMQRARKKIAECILGSNPOLT 540  
 Db 481 GILNGMPISILYNKFSDYYSKLAKAYEYTIRRERGEVNFMQRARKKIAECILGSNPOLT 540  
 QY 541 PRQEN 545  
 Db 541 PRQEN 545  
 QY 541 PRQEN 545  
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**RESULT 2**

HUMAN PRELIMINARY; PRT; 545 AA.

ID 0576X0 HUMAN PRELIMINARY; PRT; 545 AA.  
 AC 0576X0;  
 DT 01-FEB-2005 (Tremblrel. 29, Created)  
 DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)  
 DE Potassium channel, subfamily V, member 2.  
 Name=KCNV2; ORFlames-RP1-526b20.3-001;  
 OS Homo sapiens (Human).  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OX NCBI\_TAXID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

Johnson C.; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL54723; CAI15124.1; -, Genomic\_DNA.  
 DR GO; GO:00116020; C:membrane; IEA.  
 DR GO; GO:005349; P:voltage-gated potassium channel complex; IEA.  
 DR GO; GO:0005612; P:transport; IEA.  
 DR GO; GO:0006613; P:potassium ion transport; IEA.  
 KW Ion transport; Tonic channel; Transmembrane; Transport.  
 SQ SSEQUENCE 545 AA; 62459 MW; 72D1/5B4C0C6B1DA CRC64;

Query Match 100.0%; Score 2872; DB 2; Length 545; Best Local Similarity 100.0%; Pred. No. 4, 7e-219; Matches 545; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MLQSERRSWSRPWTNEESQHRSICSGARGSQASIGHWEGNWYLED 60  
 Db 1 MLQSERRSWSRPWTNEESQHRSICSGARGSQASIGHWEGNWYLED 60  
 QY 61 GEEDQWDQDQDQDQGEGVTAKPGSPDPALLSTLNNGHGSYOLDPCELAGFPK 120  
 Db 61 GEEDQWDQDQDQGEGVTAKPGSPDPALLSTLNNGHGSYOLDPCELAGFPK 120  
 QY 121 TRIGLATSTSRSRQLSCDPEQTDYFPRDPAVQVNFYUSGVLVLDGLCPRR 180  
 Db 121 TRIGLATSTSRSRQLSCDPEQTDYFPRDPAVQVNFYUSGVLVLDGLCPRR 180  
 181 FLEELGYWGRVLRKYTPRCCRCFEEERDESERLKLQHELAQAOQEAEELFRDMRFYG 240

Db 181 FLEELGYWGRVLRKYTPRCCRCFEEERDESERLKLQHELAQAOQEAEELFRDMRFYG 240  
 QY 241 PORRLMLMKPFPSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300  
 Db 241 PORRLMLMKPFPSSVAAKAGVASSFTPVLYSVVALNTVEEMQHSGCGEGFDLRP 300  
 QY 301 ILEHVELCMGFFTLEYLLASTPDIRFARSALNLVLDVAILPLXJQLLBCFTGEH 360  
 Db 301 ILEHVELCMGFFTLEYLLASTPDIRFARSALNLVLDVAILPLXJQLLBCFTGEH 360  
 QY 361 ORGOTGVSGVKQVLRLMRIRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420  
 Db 361 ORGOTGVSGVKQVLRLMRIRIKLARHSTGLRAGFTLRCYQQGCLLFIAM 420  
 QY 421 GIFTPSAVSVEHDVPSNTFTIPHSWWMAVSISVGSDMYPETHLGRFAFLCAF 480  
 Db 421 GIFTPSAVSVEHDVPSNTFTIPHSWWMAVSISVGSDMYPETHLGRFAFLCAF 480  
 QY 481 GILNGMPISILYNKFSDYYSKLAKAYEYTIRRERGEVNFMQRARKKIAECILGSNPOLT 540  
 Db 481 GILNGMPISILYNKFSDYYSKLAKAYEYTIRRERGEVNFMQRARKKIAECILGSNPOLT 540  
 QY 541 PRQEN 545  
 Db 541 PRQEN 545  
 QY 541 PRQEN 545  
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**RESULT 3**

MOUSE PRELIMINARY; PRT; 562 AA.

ID 08CF56\_MOUSE PRELIMINARY; PRT; 562 AA.  
 AC 08CF56;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DE Potassium channel, subfamily V, member 2 (Kv1.1 modulatory voltage-dependent potassium channel).  
 Name=KCNV2;  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

TISSUE=Eye; TISSUE=Eye;

DR MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sheimmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bletow K.H., Schaeffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.N., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabarrot T.L., Schatz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman J.M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,  
 RA Schniech A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002);  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Eye;  
 RC STRAIN=Eye;  
 RA Submitter (NOV-2-2002) to the EMBL/GenBank/DBJ databases.  
 RL [3]

GenCore version 5.1.7  
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## On protein - protein search, using sw model

Run on: February 7, 2006, 20:41:31 ; Search time 45 Seconds  
(without alignments)  
1165.292 Million cell updates/sec

Title: US-10-815-297-3  
Perfect score: 2872  
Sequence: 1 MLLQSERRRWSYRPWNTE.....KKIAECLIGSNPQLTPRQEN 545

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 SEQB, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%  
Maximum Match 100%

Listing first 500 summaries

Database :

PIR\_80:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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No matches found

Search completed: February 7, 2006, 20:46:19  
Job time : 45 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

February 7, 2006, 20:37:46 ; Search time 197 Seconds

1215.540 Million cell updates/sec

Title:

US-10-815-297-3

Perfect score:

2872

Sequence:

1 MLKQSERRSWSYRPWNTE.....KKTAECILGSNPOLTPRQEN 545

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

2443163 seqs, 439308781 residues

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 60%  
Maximum Match 100%  
Listing first 500 summaries

Database : A\_Geneseq\_21;\*

- 1: geneseq1980s;\*
- 2: geneseqp1990s;\*
- 3: geneseqp2000s;\*
- 4: geneseqp2001s;\*
- 5: geneseqp2002s;\*
- 6: geneseqp2003as;\*
- 7: geneseqp2003bs;\*
- 8: geneseqp2004as;\*
- 9: geneseqp2005as;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. score Query Length DB ID Description

Match Length

DB

ID

Description

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QY	1	MILQSERRSYSRPNTTENGSQHRSISLGARGSGQSISHGWTGEGNYYIEBEDD	PA (FARB ) BAYER AG.
Db	1	MILQSERRSYSRPNTTENGSQHRSISLGARGSGQSISHGWTGEGNYYIEBEDD	XX
QY	61	GEEBDQWKKDDLAEDQDAGEVTTAKPGPSDPPALLSTLNNGGHSYQDYLCELAGFPK	PT Xiao Y;
Db	61	GEEBDQWKKDDLAEDQDAGEVTTAKPGPSDPPALLSTLNNGGHSYQDYLCELAGFPK	XX
QY	121	TRIGRLATSTSRSRQLSLCDDYEEQTDYEFDRDPAVOLVNFYLSGVLLVLDGLCPRR	DR WPI: 2002-583653/62.
Db	121	TRIGRLATSTSRSRQLSLCDDYEEQTDYEFDRDPAVOLVNFYLSGVLLVLDGLCPRR	N-PSDB; ABK89197.
QY	181	FLEELGIVGVLKVTPRCCPRCIFBERDELSERIKOHELLRAQAQTEAEELFRDRHYG	DR
Db	181	FLEELGIVGVLKVTPRCCPRCIFBERDELSERIKOHELLRAQAQTEAEELFRDRHYG	XX
QY	241	PQRRLWNLMEKPFSVAAKAGIGVASSTFLVSVVALANTVEMQHSGCGEGGDLP	XX
Db	241	PQRRLWNLMEKPFSVAAKAGIGVASSTFLVSVVALANTVEMQHSGCGEGGDLP	Claim 25; Fig 6; 139pp; English.
QY	301	IIEHVNLCMGPFTLLEVLRLASTPDRRARSALNVDLVAIPLYLQIICFTGEGH	CC
Db	301	IIEHVNLCMGPFTLLEVLRLASTPDRRARSALNVDLVAIPLYLQIICFTGEGH	The invention describes a purified human voltage gated potassium channel protein KV2.2 and
QY	361	ORGOTVSVGKGQVLRMLIRFLKLARHSTGLRAGFTLRCYQQGCLLFIAM	CC protein KV2.2 (II). (I) and the polynucleotide encoding it (II) are useful for
Db	361	ORGOTVSVGKGQVLRMLIRFLKLARHSTGLRAGFTLRCYQQGCLLFIAM	CC screening for agents (III) which modify the activity of KV2.2 and
QY	421	GIFTFSAVYSVEHDVSTNTTIPHSWWMAVSISTVGIGDMYPERHLGRPAFLCAF	CC (II) for detecting a polynucleotide encoding a KV2.2 in a biological
Db	421	GIFTFSAVYSVEHDVSTNTTIPHSWWMAVSISTVGIGDMYPERHLGRPAFLCAF	sample. (III) is useful for treating a KV2.2 dysfunction related disease,
QY	421	GIFTFSAVYSVEHDVSTNTTIPHSWWMAVSISTVGIGDMYPERHLGRPAFLCAF	CC such as diabetes, cancer, peripheral or central nervous system (CNS)
Db	421	GIFTFSAVYSVEHDVSTNTTIPHSWWMAVSISTVGIGDMYPERHLGRPAFLCAF	CC disorders, or cardiovascular disorders. The CNS disorders treatable
QY	480	481 GILNGMPISIILNKFDYYSKUKAYETTIRRBERGENUFMORARKKIAECLGLSPOLT	CC include brain injuries, cerebrovascular diseases, Parkinson's disease, Alzheimer's
Db	480	481 GILNGMPISIILNKFDYYSKUKAYETTIRRBERGENUFMORARKKIAECLGLSPOLT	CC disease, vascular dementia, Parkinson linked to chromosome 17, Pick's
QY	540	541 PROEN 545	CC disease, Huntington's disease, Crutfield-Jacob dementia, schizophrenia
Db	540	541 PROEN 545	CC with dementia, attention deficit disorders; pain associated with CNS
RESULT 2			CC disorders such as multiple sclerosis, spinal cord injury, traumatic brain
ID	ABG30991		CC injury, epilepsy, human immunodeficiency virus (HIV) acquired
ID	ABG30991	standard; protein: 545 AA.	CC immunodeficiency syndrome (AIDS) related pain, cancer pain, metabolic
AC	ABG30991;		CC neuropathies, headache pain (e.g. migraine), chronic Paroxysmal
DT	21-OCT-2002	(first entry)	CC hemiplegia and tension-type like headache. Cardiovascular Diseases
DE	Human voltage gated potassium channel KV2.2.		CC treatable include congestive heart failure, myocardial infarction,
XX	Voltage gated potassium channel; KV2.2; diabetes; cancer; Pick's disease; peripheral disorder; central nervous system disorder; multiple sclerosis; cardiovascular disorder; brain injury; cerebrovascular disease; stroke; Parkinson's disease; traumatic brain injury; dementia; pain; Alzheimer's disease; Huntington's disease; Creutzfeldt-Jacob dementia; schizophrenia; attention deficit disorder; spinal cord injury; epilepsy; human immunodeficiency virus; HIV; acquired immunodeficiency syndrome; AIDS; metabolic neuropathy; chronic paroxysmal hemiplegia; headache; migraine; congestive heart failure; myocardial infarction; ischaemia; arrhythmia; vascular disease; human.		CC ischemic disease of the heart, all kinds of atrial and ventricular
OS	Homo sapiens.		CC arrhythmias, hypertensive and peripheral vascular diseases. This is the
XX	WO200255556-A2.		CC amino acid sequence of human voltage gated potassium channel KV2.2.
QY	540	Sequence 545 AA;	CC
QY	540	Query Match 100.0%; Score 2872; DB 5; Length 545;	Sequence 545 AA;
		Best Local Similarity 100.0%; Pred. No. 4.e-291;	
		Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MILQSERRSYSRPNTTENGSQHRSISLGARGSGQSISHGWTGEGNYYIEBEDD	XX
Db	1	MILQSERRSYSRPNTTENGSQHRSISLGARGSGQSISHGWTGEGNYYIEBEDD	XIAO Y;
QY	61	GEEBDQWKKDDLAEDQDAGEVTTAKPGPSDPPALLSTLNNGGHSYQDYLCELAGFPK	XX
Db	61	GEEBDQWKKDDLAEDQDAGEVTTAKPGPSDPPALLSTLNNGGHSYQDYLCELAGFPK	WPI: 2002-583653/62.
QY	121	TRIGRLATSTSRSRQLSLCDDYEEQTDYEFDRDPAVOLVNFYLSGVLLVLDGLCPRR	N-PSDB; ABK89197.
Db	121	TRIGRLATSTSRSRQLSLCDDYEEQTDYEFDRDPAVOLVNFYLSGVLLVLDGLCPRR	XX
QY	181	FLEELGIVGVLKVTPRCCPRCIFBERDELSERIKOHELLRAQAQTEAEELFRDRHYG	XX
Db	181	FLEELGIVGVLKVTPRCCPRCIFBERDELSERIKOHELLRAQAQTEAEELFRDRHYG	XX
QY	241	PQRRLWNLMEKPFSVAAKAGIGVASSTFLVSVVALANTVEMQHSGCGEGGDLP	XX
Db	241	PQRRLWNLMEKPFSVAAKAGIGVASSTFLVSVVALANTVEMQHSGCGEGGDLP	XX
QY	361	ORGOTVSVGKGQVLRMLIRFLKLARHSTGLRAGFTLRCYQQGCLLFIAM	XX
Db	361	ORGOTVSVGKGQVLRMLIRFLKLARHSTGLRAGFTLRCYQQGCLLFIAM	XX
Db	361	ORGOTVSVGKGQVLRMLIRFLKLARHSTGLRAGFTLRCYQQGCLLFIAM	XX
QY	421	GIFTFSAVYSVEHDVSTNTTIPHSWWMAVSISTVGIGDMYPERHLGRPAFLCAF	XX
Db	421	GIFTFSAVYSVEHDVSTNTTIPHSWWMAVSISTVGIGDMYPERHLGRPAFLCAF	XX